

# SEQUENCE LISTING

<110> Allan, Bernard  
 Gregoire, Francine  
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 Moodie, Shonna  
 Waters, Steve  
 Wong, Chi-Wai  
 Metabolex, Inc.

<120> Methods of Diagnosing & Treating Diabetes and Insulin  
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```

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<210> 8
<211> 553
<212> PRT
<213> Homo sapiens

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```

<220>
<223> human p21 activated kinase 1B (PAK1B) splice
variant

```

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<400> 8
Met Ser Asn Asn Gly Leu Asp Ile Gln Asp Lys Pro Pro Ala Pro Pro
 1             5             10            15

Met Arg Asn Thr Ser Thr Met Ile Gly Val Gly Ser Lys Asp Ala Gly
          20            25            30

Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
 35             40            45

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
 50             55            60

Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
 65             70            75            80

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Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe  
85 90 95  
Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile  
100 105 110  
Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu  
115 120 125  
Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser  
130 135 140  
Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Ala Leu Asn  
145 150 155 160  
Val Lys Ala Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp  
165 170 175  
Glu Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro  
180 185 190  
Arg Pro Glu His Thr Lys Ser Val Tyr Thr Arg Ser Val Ile Glu Pro  
195 200 205  
Leu Pro Val Thr Pro Thr Arg Asp Val Ala Thr Ser Pro Ile Ser Pro  
210 215 220  
Thr Glu Asn Asn Thr Thr Pro Pro Asp Ala Leu Thr Arg Asn Thr Glu  
225 230 235 240  
Lys Gln Lys Lys Lys Pro Lys Met Ser Asp Glu Glu Ile Leu Glu Lys  
245 250 255  
Leu Arg Ser Ile Val Ser Val Gly Asp Pro Lys Lys Lys Tyr Thr Arg  
260 265 270  
Phe Glu Lys Ile Gly Gln Gly Ala Ser Gly Thr Val Tyr Thr Ala Met  
275 280 285  
Asp Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln  
290 295 300  
Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg  
305 310 315 320  
Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val  
325 330 335  
Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu  
340 345 350  
Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala  
355 360 365  
Val Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln  
370 375 380  
Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp  
385 390 395 400

Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro  
 405 410 415  
 Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala  
 420 425 430  
 Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp  
 435 440 445  
 Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr  
 450 455 460  
 Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly  
 465 470 475 480  
 Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp  
 485 490 495  
 Phe Leu Asn Arg Cys Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala  
 500 505 510  
 Lys Glu Leu Leu Gln Val Arg Lys Leu Arg Phe Gln Val Phe Ser Asn  
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 Gln Pro His Ser Thr Asp Cys Cys Ser  
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<210> 9

<211> 1347

<212> DNA

<213> Homo sapiens

<220>

<223> human p21 activated kinase 1B (PAK1B) new splice variant

<400> 9

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 cctccaaacc cagaggagaa gaaaaagaag gaccgatatt accgatccat ttacctgga 180  
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 gaacacacaa ttcattgtcg ttttgatgct gtcacagggg agtttacggg aatgccagag 300  
 cagtgggccc gcttgcttca gacatcaaat atcactaagt cggagcagaa gaaaaaccg 360  
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catcaattcc tgaagattgc caagcccttc tccagcctca ctccactgat tgctgcagct 1320
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<210> 10

<211> 449

<212> PRT

<213> Homo sapiens

<220>

<223> human p21 activated kinase 1B (PAK1B) new splice  
variant

<400> 10

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Met Ser Asn Asn Gly Leu Asp Ile Gln Asp Lys Pro Pro Ala Pro Pro
  1              5              10              15

```

```

Met Arg Asn Thr Ser Thr Met Ile Gly Ala Gly Ser Lys Asp Ala Gly
          20              25              30

```

```

Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
          35              40              45

```

```

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
          50              55              60

```

```

Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
          65              70              75              80

```

```

Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
          85              90              95

```

```

Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
          100              105              110

```

```

Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
          115              120              125

```

```

Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser
          130              135              140

```

```

Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Ala Leu Asn
          145              150              155              160

```

```

Val Lys Ala Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
          165              170              175

```

```

Glu Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro
          180              185              190

```

```

Arg Pro Glu His Thr Lys Ser Val Ala Ile Lys Gln Met Asn Leu Gln
          195              200              205

```

```

Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
          210              215              220

```

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Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
          225              230              235              240

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Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu  
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 Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala  
                             260                            265                            270  
 Val Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln  
                             275                            280                            285  
 Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp  
                             290                            295                            300  
 Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro  
 305                            310                            315                            320  
 Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala  
                             325                            330                            335  
 Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp  
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 Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr  
                             355                            360                            365  
 Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly  
                             370                            375                            380  
 Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp  
 385                            390                            395                            400  
 Phe Leu Asn Arg Cys Leu Gly Met Asp Val Glu Lys Arg Gly Ser Ala  
                             405                            410                            415  
 Lys Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys Pro Leu Ser  
                             420                            425                            430  
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His

<210> 11  
 <211> 1977

<212> DNA

<213> Mus musculus

<220>

<223> mouse p21 (CDKN1A)-activated kinase 1B (PAK1B)  
 cDNA

<220>

<221> CDS

<222> (190)..(1827)

<223> PAK1B

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 cgagactcac agatacacia gatacagccc cgcacccacc gccagtagct gctgctgctg 180  
 gtggtgacaa tgtcaaataa cggcgtagac atccaggaca aacccccagc ccctccgatg 240

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<210> 12

<211> 545

<212> PRT

<213> Mus musculus

<220>

<223> mouse p21 (CDKN1A)-activated kinase 1B (PAK1B)

<400> 12

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Met Ser Asn Asn Gly Val Asp Ile Gln Asp Lys Pro Pro Ala Pro Pro
  1                      5                      10                      15

```

```

Met Arg Asn Thr Ser Thr Met Ile Gly Ala Gly Ser Lys Asp Thr Gly
          20                      25                      30

```

```

Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
          35                      40                      45

```

```

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
          50                      55                      60

```

```

Asn Lys Lys Arg Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
          65                      70                      75                      80

```

```

Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
          85                      90                      95

```

```

Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
          100                      105                      110

```

Thr	Lys	Ser	Glu	Gln	Lys	Lys	Asn	Pro	Gln	Ala	Val	Leu	Asp	Val	Leu		
		115					120						125				
Glu	Phe	Tyr	Asn	Ser	Lys	Lys	Thr	Ser	Asn	Ser	Lys	Lys	Tyr	Met	Ser		
	130					135						140					
Phe	Thr	Asp	Lys	Ser	Ala	Glu	Asp	Tyr	Asn	Ser	Ser	Asn	Thr	Leu	Asn		
145					150					155					160		
Val	Lys	Thr	Val	Ser	Glu	Thr	Pro	Ala	Val	Pro	Pro	Val	Ser	Glu	Asp		
				165					170					175			
Asp	Glu	Asp	Asp	Asp	Asp	Asp	Ala	Thr	Pro	Pro	Pro	Val	Ile	Ala	Pro		
			180					185					190				
Arg	Pro	Glu	His	Thr	Lys	Ser	Val	Tyr	Thr	Arg	Ser	Val	Ile	Glu	Pro		
		195					200					205					
Leu	Pro	Val	Thr	Pro	Thr	Arg	Asp	Val	Ala	Thr	Ser	Pro	Ile	Ser	Pro		
	210					215						220					
Thr	Glu	Asn	Asn	Thr	Thr	Pro	Pro	Asp	Ala	Leu	Thr	Arg	Asn	Thr	Glu		
225					230					235					240		
Lys	Gln	Lys	Lys	Lys	Pro	Lys	Met	Ser	Asp	Glu	Glu	Ile	Leu	Glu	Lys		
				245					250					255			
Leu	Arg	Ser	Ile	Val	Ser	Val	Gly	Asp	Pro	Lys	Lys	Lys	Tyr	Thr	Pro		
			260					265					270				
Phe	Glu	Lys	Ile	Gly	Gln	Gly	Ala	Ser	Gly	Thr	Val	Tyr	Thr	Ala	Met		
		275					280						285				
Asp	Val	Ala	Thr	Gly	Gln	Glu	Val	Ala	Ile	Lys	Gln	Met	Asn	Leu	Gln		
	290					295					300						
Gln	Gln	Pro	Lys	Lys	Glu	Leu	Ile	Ile	Asn	Glu	Ile	Leu	Val	Met	Arg		
305					310					315				320			
Glu	Asn	Lys	Asn	Pro	Asn	Ile	Val	Asn	Tyr	Leu	Asp	Ser	Tyr	Leu	Val		
				325					330					335			
Gly	Asp	Glu	Leu	Trp	Val	Val	Met	Glu	Tyr	Leu	Ala	Gly	Gly	Ser	Leu		
			340					345					350				
Thr	Asp	Val	Val	Thr	Glu	Thr	Cys	Met	Asp	Glu	Gly	Gln	Ile	Ala	Ala		
		355					360					365					
Val	Cys	Arg	Glu	Cys	Leu	Gln	Ala	Leu	Glu	Phe	Leu	His	Ser	Asn	Gln		
		370				375					380						
Val	Ile	His	Arg	Asp	Ile	Lys	Ser	Asp	Asn	Ile	Leu	Leu	Gly	Met	Asp		
385					390					395				400			
Gly	Ser	Val	Lys	Leu	Thr	Asp	Phe	Gly	Phe	Cys	Ala	Gln	Ile	Thr	Pro		
				405					410					415			
Glu	Gln	Ser	Lys	Arg	Ser	Thr	Met	Val	Gly	Thr	Pro	Tyr	Trp	Met	Ala		
			420					425					430				

Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp  
435 440 445

Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu Pro Pro Tyr  
450 455 460

Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly  
465 470 475 480

Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp  
485 490 495

Phe Leu Gln Cys Cys Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala  
500 505 510

Lys Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys Pro Leu Ser  
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His  
545

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<212> DNA  
<213> Rattus norvegicus

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<220>  
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<222> (389)..(2023)  
<223> PAK1B

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<210> 14
<211> 544
<212> PRT
<213> Rattus norvegicus

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<220>
<223> rat p21 (CDKN1A)-activated kinase 1B (PAK1B)

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Met Arg Asn Thr Ser Thr Met Ile Gly Ala Gly Ser Lys Asp Pro Gly
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Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
  35              40              45

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Ala Gly Asp Lys Thr
  50              55              60

Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
  65              70              75              80

Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
          85              90              95

Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
  100              105              110

Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
  115              120              125

Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser
  130              135              140

Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Thr Leu Asn
  145              150              155              160

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Val	Lys	Thr	Val	Ser	Glu	Thr	Pro	Ala	Val	Pro	Pro	Val	Ser	Glu	Asp	165	170	175
Glu	Asp	Asp	Asp	Asp	Asp	Ala	Thr	Pro	Pro	Pro	Val	Ile	Ala	Pro	Arg	180	185	190
Pro	Glu	His	Thr	Lys	Ser	Val	Tyr	Thr	Arg	Ser	Val	Ile	Glu	Pro	Leu	195	200	205
Pro	Val	Thr	Pro	Thr	Arg	Asp	Val	Ala	Thr	Ser	Pro	Ile	Ser	Pro	Thr	210	215	220
Glu	Asn	Asn	Thr	Thr	Pro	Pro	Asp	Ala	Leu	Thr	Arg	Asn	Thr	Glu	Lys	225	230	235
Gln	Lys	Lys	Lys	Pro	Lys	Met	Ser	Asp	Glu	Glu	Ile	Leu	Glu	Lys	Leu	245	250	255
Arg	Ser	Ile	Val	Ser	Val	Gly	Asp	Pro	Lys	Lys	Lys	Tyr	Thr	Arg	Phe	260	265	270
Glu	Lys	Ile	Gly	Gln	Gly	Ala	Ser	Gly	Thr	Val	Tyr	Thr	Ala	Met	Asp	275	280	285
Val	Ala	Thr	Gly	Gln	Glu	Val	Ala	Ile	Lys	Gln	Met	Asn	Leu	Gln	Gln	290	295	300
Gln	Pro	Lys	Lys	Glu	Leu	Ile	Ile	Asn	Glu	Ile	Leu	Val	Met	Arg	Glu	305	310	315
Asn	Lys	Asn	Pro	Asn	Ile	Val	Asn	Tyr	Leu	Asp	Ser	Tyr	Leu	Val	Gly	325	330	335
Asp	Glu	Leu	Trp	Val	Val	Met	Glu	Tyr	Leu	Ala	Gly	Gly	Ser	Leu	Thr	340	345	350
Asp	Val	Val	Thr	Glu	Thr	Cys	Met	Asp	Glu	Gly	Gln	Ile	Ala	Ala	Val	355	360	365
Cys	Arg	Glu	Cys	Leu	Gln	Ala	Leu	Glu	Phe	Leu	His	Ser	Asn	Gln	Val	370	375	380
Ile	His	Arg	Asp	Ile	Lys	Ser	Asp	Asn	Ile	Leu	Leu	Gly	Met	Asp	Gly	385	390	395
Ser	Val	Lys	Leu	Thr	Asp	Phe	Gly	Phe	Cys	Ala	Gln	Ile	Thr	Pro	Glu	405	410	415
Gln	Ser	Lys	Arg	Ser	Thr	Met	Val	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	420	425	430
Glu	Val	Val	Thr	Arg	Lys	Ala	Tyr	Gly	Pro	Lys	Val	Asp	Ile	Trp	Ser	435	440	445
Leu	Gly	Ile	Met	Ala	Ile	Glu	Met	Ile	Glu	Gly	Glu	Pro	Pro	Tyr	Leu	450	455	460
Asn	Glu	Asn	Pro	Leu	Arg	Ala	Leu	Tyr	Leu	Ile	Ala	Thr	Asn	Gly	Thr	465	470	475

Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile Phe Arg Asp Phe  
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Leu Asn Arg Cys Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala Lys  
500 505 510

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<213> Homo sapiens

<220>  
<223> human SPUVE serine protease 23 cDNA

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<222> (121) .. (1272)  
<223> SPUVE

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<211> 383  
<212> PRT  
<213> Homo sapiens

<220>

<223> human SPUVE serine protease 23

<400> 16

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		20					25					30			
Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	Leu	Asn	Leu
		35				40					45				
Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	Val	Ser	Ser	Ser
	50				55					60					
Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	Pro	Thr	Tyr	Glu	Glu
65				70				75						80	
Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	Tyr	Ala	Asn	Gly	Ser	Arg
			85					90					95		
Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile	Leu	Ser	Ser	Ser	Gly	Asp	Gly
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Gln	Ile	Tyr	Gly	Tyr	Asp	Ser	Arg	Phe	Ser	Ile	Phe	Gly	Lys	Asp	Phe
	130				135					140					
Leu	Leu	Asn	Tyr	Pro	Phe	Ser	Thr	Ser	Val	Lys	Leu	Ser	Thr	Gly	Cys
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Thr	Gly	Thr	Leu	Val	Ala	Glu	Lys	His	Val	Leu	Thr	Ala	Ala	His	Cys
			165				170						175		
Ile	His	Asp	Gly	Lys	Thr	Tyr	Val	Lys	Gly	Thr	Gln	Lys	Leu	Arg	Val
		180					185					190			
Gly	Phe	Leu	Lys	Pro	Lys	Phe	Lys	Asp	Gly	Gly	Arg	Gly	Ala	Asn	Asp
	195					200					205				
Ser	Thr	Ser	Ala	Met	Pro	Glu	Gln	Met	Lys	Phe	Gln	Trp	Ile	Arg	Val
	210				215						220				
Lys	Arg	Thr	His	Val	Pro	Lys	Gly	Trp	Ile	Lys	Gly	Asn	Ala	Asn	Asp
225				230					235					240	
Ile	Gly	Met	Asp	Tyr	Asp	Tyr	Ala	Leu	Leu	Glu	Leu	Lys	Lys	Pro	His
		245					250							255	
Lys	Arg	Lys	Phe	Met	Lys	Ile	Gly	Val	Ser	Pro	Pro	Ala	Lys	Gln	Leu
		260					265						270		
Pro	Gly	Gly	Arg	Ile	His	Phe	Ser	Gly	Tyr	Asp	Asn	Asp	Arg	Pro	Gly
	275					280						285			
Asn	Leu	Val	Tyr	Arg	Phe	Cys	Asp	Val	Lys	Asp	Glu	Thr	Tyr	Asp	Leu
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Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val  
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 Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile  
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 Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro  
 340 345 350  
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 <211> 1936  
 <212> DNA  
 <213> Mus musculus

<220>  
 <223> mouse SPUVE serine protease 23 cDNA

<220>  
 <221> CDS  
 <222> (170)..(1318)  
 <223> SPUVE

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 <211> 382  
 <212> PRT  
 <213> Mus musculus

<220>  
 <223> mouse SPUVE serine protease 23

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 Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu Ala  
 35 40 45  
 Lys Ala Asp Phe Asp Ala Lys Ala Lys Leu Glu Val Ser Ser Ser Cys  
 50 55 60  
 Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu Ala  
 65 70 75 80  
 Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg Thr  
 85 90 95  
 Glu Thr Arg Val Gly Ile Tyr Ile Leu Ser Asn Gly Glu Gly Arg Ala  
 100 105 110  
 Arg Gly Arg Asp Ser Glu Ala Thr Gly Arg Ser Arg Arg Lys Arg Gln  
 115 120 125  
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 130 135 140  
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 145 150 155 160  
 Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile  
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 His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly  
 180 185 190  
 Phe Leu Lys Pro Lys Tyr Lys Asp Gly Ala Gly Gly Asp Asn Ser Ser  
 195 200 205  
 Ser Ser Ala Met Pro Asp Lys Met Lys Phe Gln Trp Ile Arg Val Lys  
 210 215 220  
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp Ile  
 225 230 235 240  
 Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His Lys  
 245 250 255

Arg Gln Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu Pro  
                   260                                  265                                  270  
 Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly Asn  
                   275                                  280                                  285  
 Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu Leu  
                   290                                  295                                  300  
 Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val Tyr  
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 Val Arg Met Trp Lys Arg Pro Gln Gln Lys Trp Glu Arg Lys Ile Ile  
                   325                                  330                                  335  
 Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro Gln  
                   340                                  345                                  350  
 Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile  
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 Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly  
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<210> 19

<211> 827

<212> DNA

<213> Homo sapiens

<220>

<223> human similar to natural killer cell transcript 4  
(NK4) cDNA

<220>

<221> CDS

<222> (59)..(625)

<223> NK4

<400> 19

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<211> 188

<212> PRT

<213> Homo sapiens

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 35 40 45  
 Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu  
 50 55 60  
 Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu  
 65 70 75 80  
 Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala  
 85 90 95  
 Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe  
 100 105 110  
 Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala  
 115 120 125  
 Trp Val Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu  
 130 135 140  
 Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met  
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 Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys  
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<210> 21  
 <211> 2254  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human Protein C inhibitor (PCI) cDNA

<220>  
 <221> CDS  
 <222> (140)..(1360)  
 <223> PCI

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<210> 22  
 <211> 406  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human Protein C inhibitor (PCI)

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 Asp Leu His Val Gly Ala Thr Val Ala Pro Ser Ser Arg Arg Asp Phe  
 35 40 45  
 Thr Phe Asp Leu Tyr Arg Ala Leu Ala Ser Ala Ala Pro Ser Gln Asn  
 50 55 60  
 Ile Phe Phe Ser Pro Val Ser Ile Ser Met Ser Leu Ala Met Leu Ser  
 65 70 75 80  
 Leu Gly Ala Gly Ser Ser Thr Lys Met Gln Ile Leu Glu Gly Leu Gly  
 85 90 95

Leu Asn Leu Gln Lys Ser Ser Glu Lys Glu Leu His Arg Gly Phe Gln  
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 Phe Val Ser Ala Met Lys Thr Leu Tyr Leu Ala Asp Thr Phe Pro Thr  
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 Ala Lys Gln Thr Lys Gly Lys Ile Val Asp Leu Leu Lys Asn Leu Asp  
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 Ser Asn Ala Val Val Ile Met Val Asn Tyr Ile Phe Phe Lys Ala Lys  
 195 200 205  
 Trp Glu Thr Ser Phe Asn His Lys Gly Thr Gln Glu Gln Asp Phe Tyr  
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 Val Thr Ser Glu Thr Val Val Arg Val Pro Met Met Ser Arg Glu Asp  
 225 230 235 240  
 Gln Tyr His Tyr Leu Leu Asp Arg Asn Leu Ser Cys Arg Val Val Gly  
 245 250 255  
 Val Pro Tyr Gln Gly Asn Ala Thr Ala Leu Phe Ile Leu Pro Ser Glu  
 260 265 270  
 Gly Lys Met Gln Gln Val Glu Asn Gly Leu Ser Glu Lys Thr Leu Arg  
 275 280 285  
 Lys Trp Leu Lys Met Phe Lys Lys Arg Gln Leu Glu Leu Tyr Leu Pro  
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 Ser Asn His Ser Asn Ile Gln Val Ser Glu Met Val His Lys Ala Val  
 340 345 350  
 Val Glu Val Asp Glu Ser Gly Thr Arg Ala Ala Ala Ala Thr Gly Thr  
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 Ile Phe Thr Phe Arg Ser Ala Arg Leu Asn Ser Gln Arg Leu Val Phe  
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 Gly Lys Val Asn Arg Pro  
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<210> 23  
 <211> 2125  
 <212> DNA  
 <213> Mus musculus

<220>  
 <223> mouse Protein C inhibitor (PCI), serine (or  
 cysteine) proteinase inhibitor, clade A, member 5  
 (Serpina5) cDNA

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 <221> CDS  
 <222> (125) .. (1342)  
 <223> PCI

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<210> 24  
 <211> 405  
 <212> PRT  
 <213> Mus musculus

<220>

<223> mouse Protein C inhibitor (PCI), serine (or  
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(Serpina5)

<400> 24

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Ala	Gly	Leu	Lys	Thr	Lys	Thr	Gln	Ile	Leu	Asp	Gly	Leu	Gly	Leu	Ser	
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Gln	Thr	Lys	Gly	Lys	Ile	Val	Asp	Leu	Ile	Lys	Asp	Leu	Asp	Ser	Thr	
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His	Val	Met	Ile	Val	Val	Asn	Tyr	Ile	Phe	Phe	Lys	Ala	Lys	Trp	Gln	
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Tyr	Gln	Gly	Asn	Ala	Ile	Ala	Leu	Phe	Ile	Leu	Pro	Ser	Glu	Gly	Lys	
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 <212> DNA  
 <213> Rattus norvegicus

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 (Serpina5) cDNA

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 <222> (48)..(1268)  
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<210> 26

<211> 406

<212> PRT

<213> Rattus norvegicus

<220>

<223> rat Protein C inhibitor (PCI), serine (or  
cysteine) proteinase inhibitor, clade A, member 5  
(Serpina5)

<400> 26

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Glu Ser Ser Val Gly Ala Val Gly Thr Ser Arg Ser Arg Asp Phe Ala
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Phe Arg Leu Tyr Arg Ala Leu Ala Ser Glu Ala Pro Gly Gln Asn Val
          50             55             60

Phe Phe Ser Pro Met Ser Val Ser Met Ser Leu Gly Met Leu Ser Leu
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Gly Ser Gly Leu Lys Thr Lys Ala Gln Ile Leu Glu Gly Leu Gly Leu
          85             90             95

Ser Leu Gln Gln Gly Gln Glu Asp Met Leu His Lys Gly Phe Gln Gln
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Leu Leu Gln Gln Phe Ser Gln Pro Ser Asp Gly Leu Gln Leu Ser Leu
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Gly Ser Ala Leu Phe Thr Asp Pro Ala Val His Ile Arg Asp His Phe
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Leu Ser Ala Met Lys Thr Leu Tyr Met Ser Asp Met Phe Ser Thr Asn
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Phe Gly Asn Pro Glu Ser Ala Lys Lys Gln Ile Asn Asp Tyr Val Ala
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Lys Lys Thr Asn Gly Lys Ile Val Asp Leu Ile Lys Asp Leu Asp Ser  
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 Pro Tyr Gln Gly Asn Thr Phe Ala Leu Phe Ile Leu Pro Ser Glu Gly  
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<211> 5073

<212> DNA

<213> Homo sapiens

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<223> human MAST205b novel variant

<220>

<221> CDS

<222> (1)..(5073)

<223> MAST205b novel variant

<400> 27

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Asn Pro Arg Ala His Ser Ser Pro Gly Thr Pro Cys Ser Ser Arg Pro
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Leu Pro Trp Ser Cys Arg Thr Ser Asn Arg Lys Ser Leu Ile Val Thr
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Ser Ser Thr Ser Pro Thr Leu Pro Arg Pro His Ser Pro Leu His Gly
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His Thr Gly Asn Ser Pro Leu Asp Ser Pro Arg Asn Phe Ser Pro Asn
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Ala Asp Arg Thr Asp Gly Arg Arg Trp Ser Leu Ala Ser Leu Pro Ser
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Ser Gly Tyr Gly Thr Asn Thr Pro Ser Ser Thr Val Ser Ser Ser Cys
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Glu	Glu	Gly	Arg	Gln	Ser	Pro	Ala	Met	Arg	Pro	Arg	Ser	Arg	Ser	Leu	
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Ser	Pro	Gly	Arg	Ser	Pro	Val	Ser	Phe	Asp	Ser	Glu	Ile	Ile	Met	Met	
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Asn	His	Val	Tyr	Lys	Glu	Arg	Phe	Pro	Lys	Ala	Thr	Ala	Gln	Met	Glu	
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Glu	Arg	Leu	Ala	Glu	Phe	Ile	Ser	Ser	Asn	Thr	Pro	Asp	Ser	Val	Leu	
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<210> 32

<211> 1734

<212> PRT

<213> Mus musculus

<220>

<223> mouse microtubule associated testis specific  
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<400> 32

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Asp	Ile	Phe	Ala	Pro	Thr	Gly	Lys	Val	Lys	Leu	Gln	Arg	Gln	Leu	Ser	20	25	30	
Gln	Asp	Asp	Cys	Lys	Leu	Arg	Arg	Gly	Ser	Leu	Ala	Ser	Ser	Leu	Ser	35	40	45	
Gly	Lys	Gln	Leu	Leu	Pro	Leu	Ser	Ser	Ser	Val	His	Ser	Ser	Val	Gly	50	55	60	
Gln	Val	Thr	Trp	Gln	Ser	Thr	Gly	Glu	Ala	Ser	Asn	Leu	Val	Arg	Met	65	70	75	80
Arg	Asn	Gln	Ser	Leu	Gly	Gln	Ser	Ala	Pro	Ser	Leu	Thr	Ala	Gly	Leu	85	90	95	
Lys	Glu	Leu	Ser	Leu	Pro	Arg	Arg	Gly	Ser	Phe	Cys	Arg	Thr	Ser	Asn	100	105	110	
Arg	Lys	Ser	Leu	Ile	Val	Thr	Ser	Ser	Thr	Ser	Pro	Thr	Leu	Pro	Arg	115	120	125	
Pro	His	Ser	Pro	Leu	His	Gly	His	Thr	Gly	Asn	Ser	Pro	Leu	Asp	Ser	130	135	140	
Pro	Arg	Asn	Phe	Ser	Pro	Asn	Ala	Pro	Ala	His	Phe	Ser	Phe	Val	Pro	145	150	155	160
Ala	Arg	Arg	Thr	Asp	Gly	Arg	Arg	Trp	Ser	Leu	Ala	Ser	Leu	Pro	Ser	165	170	175	
Ser	Gly	Tyr	Gly	Thr	Asn	Thr	Pro	Ser	Ser	Thr	Val	Ser	Ser	Ser	Cys	180	185	190	
Ser	Ser	Gln	Glu	Lys	Leu	His	Gln	Leu	Pro	Phe	Gln	Pro	Thr	Ala	Asp	195	200	205	
Glu	Leu	His	Phe	Leu	Thr	Lys	His	Phe	Ser	Thr	Glu	Asn	Val	Pro	Asp	210	215	220	
Glu	Glu	Gly	Arg	Arg	Ser	Pro	Arg	Met	Arg	Pro	Arg	Ser	Arg	Ser	Leu	225	230	235	240



Ser	Pro	Gly	Arg	Ser	Pro	Val	Ser	Phe	Asp	Ser	Glu	Ile	Ile	Met	Met	
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Glu	Met	Ala	Arg	Asp	Cys	Leu	Asp	Lys	Ser	Arg	Ser	Gly	Leu	Ile	Thr	
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Glu	Cys	Leu	Glu	Phe	Asp	Pro	Glu	Glu	Phe	Tyr	His	Leu	Leu	Glu	Ala	
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Ile	Gly	Ala	Leu	Pro	Val	Asp	Met	Val	Arg	Leu	Tyr	Phe	Ala	Glu	Thr	
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Val	Leu	Ala	Leu	Glu	Tyr	Leu	His	Asn	Tyr	Gly	Ile	Val	His	Arg	Asp	
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His	Gln	Asn	Pro	Leu	Glu	Arg	Leu	Gly	Thr	Ser	Ser	Ala	Tyr	Glu	Val	
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Gln	Lys	Ala	Glu	Phe	Ile	Pro	Gln	Leu	Glu	Ser	Glu	Asp	Asp	Thr	Ser	
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Gln	Ser 930	Ser	Arg	Cys	Cys	Pro 935	Ala	Leu	Glu	Thr	Arg 940	Gly	Arg	Gly	Thr
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Arg	Thr	Thr	Arg 980	Pro	Val	Asn	Lys	Val 985	Ile	Lys	Ser	Ala	Ser 990	Ala	Thr
Ala	Leu	Ser 995	Leu	Leu	Ile	Pro 1000	Ser	Glu	His	His	Ala	Cys 1005	Ser	Pro	Leu
Ala 1010	Ser	Pro	Met	Ser	Pro 1015	His	Ser	Gln	Ser	Ser	Asn 1020	Pro	Ser	Ser	Arg
Asp 1025	Ser	Ser	Pro	Ser	Arg 1030	Asp	Phe	Leu	Pro	Ala 1035	Leu	Gly	Ser	Leu 1040	Arg
Pro	Pro	Ile	Ile 1045	Ile	His	Arg	Ala	Gly	Lys 1050	Lys	Tyr	Gly	Phe	Thr 1055	Leu
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Lys	Arg 1155	Ser	Lys	Gly	Lys	Asp	Gly 1160	Gln	Glu	Ser	Arg	Lys 1165	Arg	Ser	Ser
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 Ser Gln Ser Ser Ser Pro Ser Ser Ser Val Pro Ser Ser Pro Ala Gly  
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 Ser Gly His Thr Arg Pro Ser Ser Leu His Gly Leu Ala Pro Lys Leu  
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<223> human colon Kruppel-like factor (CKLF) cDNA

<220>

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<223> CKLF

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<220>  
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 Val Leu Gly Ala Ala Asn Pro Ala Arg Asp Ala Ala Leu Phe Pro Gly  
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 Glu Glu Leu Lys His Ala His His Arg Pro Gln Ala Gln Pro Ala Pro  
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 Ala Gln Ala Pro Gln Pro Ala Gln Pro Pro Ala Thr Gly Pro Arg Leu  
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 Pro Pro Glu Asp Leu Val Gln Thr Arg Cys Glu Met Glu Lys Tyr Leu  
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 Thr Pro Gln Leu Pro Pro Val Pro Ile Ile Pro Glu His Lys Lys Tyr  
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 Arg Arg Asp Ser Ala Ser Val Val Asp Gln Phe Phe Thr Asp Thr Glu  
           115                  120                  125  
 Gly Leu Pro Tyr Ser Ile Asn Met Asn Val Phe Leu Pro Asp Ile Thr  
           130                  135                  140  
 His Leu Arg Thr Gly Leu Tyr Lys Ser Gln Arg Pro Cys Val Thr His  
           145                  150                  155                  160  
 Ile Lys Thr Glu Pro Val Ala Ile Phe Ser His Gln Ser Glu Thr Thr  
                   165                  170                  175  
 Ala Pro Pro Pro Ala Pro Thr Gln Ala Leu Pro Glu Phe Thr Ser Ile  
                   180                  185                  190  
 Phe Ser Ser His Gln Thr Ala Ala Pro Glu Val Asn Asn Ile Phe Ile  
           195                  200                  205  
 Lys Gln Glu Leu Pro Thr Pro Asp Leu His Leu Ser Val Pro Thr Gln  
           210                  215                  220  
 Gln Gly His Leu Tyr Gln Leu Leu Asn Thr Pro Asp Leu Asp Met Pro  
           225                  230                  235                  240  
 Ser Ser Thr Asn Gln Thr Ala Ala Met Asp Thr Leu Asn Val Ser Met  
                   245                  250                  255  
 Ser Ala Ala Met Ala Gly Leu Asn Thr His Thr Ser Ala Val Pro Gln  
                   260                  265                  270

Thr Ala Val Lys Gln Phe Gln Gly Met Pro Pro Cys Thr Tyr Thr Met  
 275 280 285  
 Pro Ser Gln Phe Leu Pro Gln Gln Ala Thr Tyr Phe Pro Pro Ser Pro  
 290 295 300  
 Pro Ser Ser Glu Pro Gly Ser Pro Asp Arg Gln Ala Glu Met Leu Gln  
 305 310 315 320  
 Asn Leu Thr Pro Pro Pro Ser Tyr Ala Ala Thr Ile Ala Ser Lys Leu  
 325 330 335  
 Ala Ile His Asn Pro Asn Leu Pro Thr Thr Leu Pro Val Asn Ser Gln  
 340 345 350  
 Asn Ile Gln Pro Val Arg Tyr Asn Arg Arg Ser Asn Pro Asp Leu Glu  
 355 360 365  
 Lys Arg Arg Ile His Tyr Cys Asp Tyr Pro Gly Cys Thr Lys Val Tyr  
 370 375 380  
 Thr Lys Ser Ser His Leu Lys Ala His Leu Arg Thr His Thr Gly Glu  
 385 390 395 400  
 Lys Pro Tyr Lys Cys Thr Trp Glu Gly Cys Asp Trp Arg Phe Ala Arg  
 405 410 415  
 Ser Asp Glu Leu Thr Arg His Tyr Arg Lys His Thr Gly Ala Lys Pro  
 420 425 430  
 Phe Gln Cys Gly Val Cys Asn Arg Ser Phe Ser Arg Ser Asp His Leu  
 435 440 445  
 Ala Leu His Met Lys Arg His Gln Asn  
 450 455

<210> 35

<211> 1591

<212> DNA

<213> Mus musculus

<220>

<223> mouse intestinal-enriched Kruppel-like factor  
(IKLF, CKLF) cDNA

<220>

<221> CDS

<222> (167)..(1507)

<223> CKLF

<400> 35

ccgagccccag gagccccgat ctccgtgccc gccttcgtga gcgtctggct gccggccccag 60  
 ggggtcccccg ccgcgggcccc ccgcgcagtc cgccgtccccg tgccagccccg agcgaggtgg 120  
 gatcgcgatc gctccgtgtc ccgctcccgat aatccccaga ccgtccatgc ccacgcgggt 180  
 gctgaccatg agcgcgccgc tgggaccact gccccagccg ccggccgcgc aggccgagcc 240  
 cgtgttcgcg cagctcaagc cgggtgctggg cgctgcgaac ccggccccgc acgcggcgct 300  
 cttctccgga gacgatctga aacacgcgca ccaccacccg cctgcgccgc cgccagccgc 360  
 tggccccgca ctgccctcgg aggagctggt ccagacaaga tgtgaaatgg agaagtatct 420  
 gaccctcag ctccctccag ttccgataat ttcagagcat aaaaagtata gacgagacag 480  
 tgcctcagtg gtagaccagt tcttcactga cactgaaggc ataccttaca gcatcaacat 540



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gaacgtotc ctccctgaca tcactcacct gagaactggc ctctacaaat cccagagacc 600
atgcgtaaca cagatcaaga cagaacctgt taccattttc agccaccaga gcgagtcgac 660
ggccccctct cctcctccgg cccccaccca ggctctcccc gagttcacta gtatcttcag 720
ctcccaccag accacagcgc caccacagga ggtgaacaat atcttcatca aacaagaact 780
tcctatacca gatcttcatc tctctgtccc tccccagcag ggccacctgt accagctgtt 840
gaatacaccg gatctagaca tgcccagttc gacaaaccag acggcagtaa tggacaccct 900
taatgtttct atggcaggcc ttaaccaca cccctctgct gtccacaga cgtcaatgaa 960
acagttccag ggcattgccc cttgcacgta caccatgcca agtcagtttc ttccacagca 1020
ggccacttat tttccccgt caccaccaag ctcagagcct ggaagtcccg atagacaagc 1080
tgagatgctg cagaatctca cccacctcc gtcctatgcc gctacaattg cttccaaact 1140
ggcgattcac aacccaaatt tacctgccac tctgccagtt aattcgccaa ctctcccacc 1200
tgtcagatac aacagaagga gtaaccgga tctggagaag cgacgtatcc acttctgcga 1260
ttataatggt tgcacaaaag tttatacaaa gtcgtctcac ttaaaagctc acctgaggac 1320
tcatacgggc gagaagccct acaagtgcac ctgggagggc tgcgactgga ggtttgcccg 1380
gtcggatgag ctgacccgcc actacaggaa gcacacgggc gccaaagccg tccagtgcac 1440
ggtgtgccaa cgcagcttct cccgtccga ccacctcgcg ctgcacatga agcgccacca 1500
gaactgagcg agcgaacgct gcgcccaccc gcctgacgcc ttgcagtcg ctttgccatc 1560
ctttaaaccc cagacctaac ttcataaaaa g 1591

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<210> 36

<211> 446

<212> PRT

<213> Mus musculus

<220>

<223> mouse intestinal-enriched Kruppel-like factor  
(IKLF, CKLF)

<400> 36

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Met Pro Thr Arg Val Leu Thr Met Ser Ala Arg Leu Gly Pro Leu Pro
 1             5             10             15

Gln Pro Pro Ala Ala Gln Ala Glu Pro Val Phe Ala Gln Leu Lys Pro
          20             25             30

Val Leu Gly Ala Ala Asn Pro Ala Arg Asp Ala Ala Leu Phe Ser Gly
          35             40             45

Asp Asp Leu Lys His Ala His His His Pro Pro Ala Pro Pro Pro Ala
 50             55             60

Ala Gly Pro Arg Leu Pro Ser Glu Glu Leu Val Gln Thr Arg Cys Glu
 65             70             75             80

Met Glu Lys Tyr Leu Thr Pro Gln Leu Pro Pro Val Pro Ile Ile Ser
          85             90             95

Glu His Lys Lys Tyr Arg Arg Asp Ser Ala Ser Val Val Asp Gln Phe
          100            105            110

Phe Thr Asp Thr Glu Gly Ile Pro Tyr Ser Ile Asn Met Asn Val Phe
          115            120            125

Leu Pro Asp Ile Thr His Leu Arg Thr Gly Leu Tyr Lys Ser Gln Arg
          130            135            140

Pro Cys Val Thr Gln Ile Lys Thr Glu Pro Val Thr Ile Phe Ser His
          145            150            155            160

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Gln Ser Glu Ser Thr Ala Pro Pro Pro Pro Pro Ala Pro Thr Gln Ala  
 165 170 175  
 Leu Pro Glu Phe Thr Ser Ile Phe Ser Ser His Gln Thr Thr Ala Pro  
 180 185 190  
 Pro Gln Glu Val Asn Asn Ile Phe Ile Lys Gln Glu Leu Pro Ile Pro  
 195 200 205  
 Asp Leu His Leu Ser Val Pro Ser Gln Gln Gly His Leu Tyr Gln Leu  
 210 215 220  
 Leu Asn Thr Pro Asp Leu Asp Met Pro Ser Ser Thr Asn Gln Thr Ala  
 225 230 235 240  
 Val Met Asp Thr Leu Asn Val Ser Met Ala Gly Leu Asn Pro His Pro  
 245 250 255  
 Ser Ala Val Pro Gln Thr Ser Met Lys Gln Phe Gln Gly Met Pro Pro  
 260 265 270  
 Cys Thr Tyr Thr Met Pro Ser Gln Phe Leu Pro Gln Gln Ala Thr Tyr  
 275 280 285  
 Phe Pro Pro Ser Pro Pro Ser Ser Glu Pro Gly Ser Pro Asp Arg Gln  
 290 295 300  
 Ala Glu Met Leu Gln Asn Leu Thr Pro Pro Pro Ser Tyr Ala Ala Thr  
 305 310 315 320  
 Ile Ala Ser Lys Leu Ala Ile His Asn Pro Asn Leu Pro Ala Thr Leu  
 325 330 335  
 Pro Val Asn Ser Pro Thr Leu Pro Pro Val Arg Tyr Asn Arg Arg Ser  
 340 345 350  
 Asn Pro Asp Leu Glu Lys Arg Arg Ile His Phe Cys Asp Tyr Asn Gly  
 355 360 365  
 Cys Thr Lys Val Tyr Thr Lys Ser Ser His Leu Lys Ala His Leu Arg  
 370 375 380  
 Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Thr Trp Glu Gly Cys Asp  
 385 390 395 400  
 Trp Arg Phe Ala Arg Ser Asp Glu Leu Thr Arg His Tyr Arg Lys His  
 405 410 415  
 Thr Gly Ala Lys Pro Phe Gln Cys Met Val Cys Gln Arg Ser Phe Ser  
 420 425 430  
 Arg Ser Asp His Leu Ala Leu His Met Lys Arg His Gln Asn  
 435 440 445

<210> 37  
 <211> 877  
 <212> DNA  
 <213> Rattus norvegicus

<220>  
 <223> rat Kruppel-like factor 5, intestinal (KLF5, CKLF)  
 cDNA

<220>  
 <221> CDS  
 <222> (145)..(792)  
 <223> CKLF

<400> 37  
 cggatatttca gctcccacca gaccacagcg ccagaggtga acaatatctt catcaaacia 60  
 gaacttctta taccagatct tcatctctcg gtcccttccc agcagggcca cctgtaccag 120  
 ctgttgaata cacctgatct agacatgccc agttcgacaa accagacagc agtcatggac 180  
 acccttaatg tctctatggc tggccttaac tcacaccctt ctgctgtgcc acagacgtcc 240  
 atgaaacagt tccagggcat gcctccttgc acgtacacca tgccgagtca gtttcttcca 300  
 cagcaggcca cctacttttc cccatcacca ccgagctcag agcctggaag tcctgataga 360  
 caagctgaga tgctccagaa tctgacccca cctccgtcct atgctgctac aattgcttcg 420  
 aaactggcaa ttcacaatcc aaatttacct gccactctgc cagttaattc gccaaatatt 480  
 caacctgtcc gataacaacag aaggagtaac ccggtatctgg agaagcgacg catccatttc 540  
 tgtgattatg atggttgac aaaagtatt acaaagtcgt ctcatthaaa agtccacctg 600  
 aggactcata cgggagagaa gccctacaag tgcacctggg agggctgcga ctggagggtt 660  
 gcccggtcgg acgagctgac ccgccactac aggaagcaca cgggtgccaa gccgttccag 720  
 tgctgtgtgt gcaaccgcag cttctccgc tccgaccacc tggcgctgca catgaagcgc 780  
 caccagaact gagcactgcg cacaaccggc tcgacgcctc gcagtcgcgt cgccatcctt 840  
 taaaccgcag acctaacttc atataaaaaa aaaaaaa 877

<210> 38  
 <211> 215  
 <212> PRT  
 <213> Rattus norvegicus

<220>  
 <223> rat Kruppel-like factor 5, intestinal (KLF5, CKLF)

<400> 38  
 Met Pro Ser Ser Thr Asn Gln Thr Ala Val Met Asp Thr Leu Asn Val  
 1 5 10 15  
 Ser Met Ala Gly Leu Asn Ser His Pro Ser Ala Val Pro Gln Thr Ser  
 20 25 30  
 Met Lys Gln Phe Gln Gly Met Pro Pro Cys Thr Tyr Thr Met Pro Ser  
 35 40 45  
 Gln Phe Leu Pro Gln Gln Ala Thr Tyr Phe Pro Pro Ser Pro Pro Ser  
 50 55 60  
 Ser Glu Pro Gly Ser Pro Asp Arg Gln Ala Glu Met Leu Gln Asn Leu  
 65 70 75 80  
 Thr Pro Pro Pro Ser Tyr Ala Ala Thr Ile Ala Ser Lys Leu Ala Ile  
 85 90 95  
 His Asn Pro Asn Leu Pro Ala Thr Leu Pro Val Asn Ser Pro Asn Ile  
 100 105 110  
 Gln Pro Val Arg Tyr Asn Arg Arg Ser Asn Pro Asp Leu Glu Lys Arg  
 115 120 125

Arg	Ile	His	Phe	Cys	Asp	Tyr	Asp	Gly	Cys	Thr	Lys	Val	Tyr	Thr	Lys
130						135					140				
Ser	Ser	His	Leu	Lys	Ala	His	Leu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro
145					150					155					160
Tyr	Lys	Cys	Thr	Trp	Glu	Gly	Cys	Asp	Trp	Arg	Phe	Ala	Arg	Ser	Asp
				165					170					175	
Glu	Leu	Thr	Arg	His	Tyr	Arg	Lys	His	Thr	Gly	Ala	Lys	Pro	Phe	Gln
			180					185					190		
Cys	Val	Val	Cys	Asn	Arg	Ser	Phe	Ser	Arg	Ser	Asp	His	Leu	Ala	Leu
		195					200					205			
His	Met	Lys	Arg	His	Gln	Asn									
210						215									

<210> 39  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:MAST205b PCR  
 Forward primer 110F

<400> 39  
 acagcagtcc tggcactcct t 21

<210> 40  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:MAST205b PCR  
 Reverse primer 174R

<400> 40  
 gcgggttactt gtccgacaac tc 22

<210> 41  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:MAST205b PCR  
 Taqman Probe Probe133

<400> 41  
 tccagccgcc cactgccg 18

<210> 42  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:MAST205 PCR  
         Forward primer 717F  
  
 <400> 42  
 ttggacagtc tgcaccttct ctta 24  
  
 <210> 43  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:MAST205 PCR  
         Reverse primer 801R  
  
 <400> 43  
 cggttacttg tccgacaaaa gc 22  
  
 <210> 44  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:MAST205 PCR  
         Taqman Probe Probe745  
  
 <400> 44  
 tggcctgaag gacttgagcc ttccagccca ctgccg 36  
  
 <210> 45  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:hexahistidine  
         (His) affinity tag  
  
 <400> 45  
 His His His His His His  
     1                    5  
  
 <210> 46  
 <211> 200  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
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         flexible linker

<220>  
 <221> MOD\_RES  
 <222> (6)..(200)  
 <223> Gly residues from position 6 to 200 may be present  
 or absent

<400> 46  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 1 5 10 15  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 20 25 30  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 35 40 45  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 50 55 60  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 65 70 75 80  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 85 90 95  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 100 105 110  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 115 120 125  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 130 135 140  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 145 150 155 160  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 165 170 175  
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 180 185 190  
 Gly Gly Gly Gly Gly Gly Gly  
 195 200